lum	ber: 09/068, \$07/H CRF Processi	/2/
Cha	anged a file from non-ASCII to ASCII Verified by: _	(STIC s
Cha	anged the margins in cases where the sequence text was "wrapped" down to the	next line.
Edit	ted a format error in the Current Application Data section, specifically: ENT	ERED
Edit app	ted the Current Application Data section with the actual current number. The number licant was  the prior application data; or other	nber inputted by the
Add	led the mandatory heading and subheadings for "Current Application Data".	
Edit	ed the "Number of Sequences" field. The applicant spelled out a number instead	d of using an integer.
Cha	anged the spelling of a mandatory field (the headings or subheadings), specifically	y:
Con	rected the SEQ ID NO when obviously incorrect. The sequence numbers that we	ere edited were:
nse	erted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's ed	lited:
Con appl	rected subheading placement. All responses must be on the same line as each s licant placed a response below the subheading, this was moved to its appropriate	subheading. If the place.
Inse	erted colons after headings/subheadings. Headings edited included:	
Del	eted extra, invalid, headings used by an applicant, specifically:	
De	leted:   non-ASCII "garbage" at the beginning/end of files;  secretary initial page numbers throughout text;  other invalid text, such as	ls/filename at end of fil
Ins	erted mandatory headings, specifically:	·
Со	rrected an obvious error in the response, specifically:	
Edi	ited identifiers where upper case is used but lower case is required, or vice versa	i.
Co	rrected an error in the Number of Sequences field, specifically:	
	Hard Page Break" code was inserted by the applicant. All occurrences had to be	
Dele due	nted <b>ending</b> stop codon in amino acid sequences and adjusted the "(A)Length:" to a Patentin bug). Sequences corrected:	field accordingly (error
Ott	ner:	

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

46

#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/068,507A

DATE: 02/18/1999 TIME: 15:34:22

INPUT SET: S30728.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

**ENTERED** SEQUENCE LISTING 1 2 General Information: (1) 3 4 (i) APPLICANT: EIJSINK, VINCENT G.H. 5 BRURBERG, MAY B. 6 NES, INGOLF F. 7 8 (ii) TITLE OF INVENTION: EXPRESSION SYSTEM IN MICROORGANISM AND 9 ITS USE FOR EXPRESSING HETEROLOGOUS AND HOMOLOGOUS 10 PROTEINS 11 12 (iii) NUMBER OF SEQUENCES: 12 13 14 (iv) CORRESPONDENCE ADDRESS: 15 (A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP 16 (B) STREET: PO BOX 747 17 (C) CITY: FALLS CHURCH 18 (D) STATE: VA 19 (E) COUNTRY: USA 20 (F) ZIP: 22040-0747 21 22 (v) COMPUTER READABLE FORM: 23 (A) MEDIUM TYPE: Floppy disk 24 (B) COMPUTER: IBM PC compatible 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 27 28 (vi) CURRENT APPLICATION DATA: 29 (A) APPLICATION NUMBER: 30 (B) FILING DATE: 31 (C) CLASSIFICATION: 32 33 (viii) ATTORNEY/AGENT INFORMATION: 34 (A) NAME: MURPHY JR., GERLAD M. 35 (B) REGISTRATION NUMBER: 28,977 36 (C) REFERENCE/DOCKET NUMBER: 1380-0122P 37 38 (ix) TELECOMMUNICATION INFORMATION: 39 (A) TELEPHONE: 703-205-8000 40 (B) TELEFAX: 703-205-8050 41 42 43 (2) INFORMATION FOR SEQ ID NO:1: 44 45 (i) SEQUENCE CHARACTERISTICS:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/068,507A

DATE: 02/18/1999 TIME: 15:34:22

INPUT SET: S30728.raw

	INPUT SET: S30728	.raw
47	(A) LENGTH: 26 amino acids	
48	(B) TYPE: amino acid	
49	(C) STRANDEDNESS: single .	
50	(D) TOPOLOGY: linear	
51		
52	(ii) MOLECULE TYPE: peptide	
53	(II) Normeon IIII. peptide	
54	(iii) HYDOMHERTAN NO	
-	(iii) HYPOTHETICAL: NO	
55		
56	(iv) ANTI-SENSE: NO	
57		
58	(v) FRAGMENT TYPE: C-terminal	
59		
60	(vi) ORIGINAL SOURCE:	
61	(A) ORGANISM: Lactobacillus platarum	
62	(B) STRAIN: C11	
63		
64		
65		
66	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
67	(AI) BEGGENCE DESCRIPTION. BEG ID NO.1.	
	The Con Con No Man Con Lon Cla Mat Cla No Mha No The The Land Cla	
68	Lys Ser Ser Ala Tyr Ser Leu Gln Met Gly Ala Thr Ala Ile Lys Gln	
69	1 5 10 15	
70		
71	Val Lys Lys Leu Phe Lys Lys Trp Gly Trp	
72	20 25	
73		
74		
75	(2) INFORMATION FOR SEQ ID NO:2:	
76		
77	(i) SEQUENCE CHARACTERISTICS:	
78	(A) LENGTH: 114 base pairs	
79	(B) TYPE: nucleic acid	
80	(C) STRANDEDNESS: single	
81	(D) TOPOLOGY: linear	
82	(b) Totologi. Timedi	
83	(ii) MOLEGULE TYPE, DNA (gonomia)	
	(ii) MOLECULE TYPE: DNA (genomic)	
84		
85	(1.4)	
86	(ix) FEATURE:	
87	(A) NAME/KEY: CDS	
88	(B) LOCATION: 1114	
89		
90		
91	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
92		
93	ATG ATG ATA TTT AAA AAA CTT TCA GAA AAA GAA TTG CAA AAA ATA AAC	48
94	Met Met Ile Phe Lys Lys Leu Ser Glu Lys Glu Leu Gln Lys Ile Asn	
95	1 5 10 15	
96		
97	GGT GGT ATG GCA GGA AAT AGT TCT AAT TTT ATT CAT AAG ATT AAA CAA	96
98	Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln	20
99	20 25 30	
23	20 25 30	

#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/068,507A

DATE: 02/18/1999 TIME: 15:34:23

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100 101 102 103 104 105	ATT TTT ACC CAT CGT TAA  Ile Phe Thr His Arg *  35	114
106	(2) INFORMATION FOR SEQ ID NO:3:	
107		
108	(i) SEQUENCE CHARACTERISTICS:	
109	(A) LENGTH: 37 amino acids	
110	(B) TYPE: amino acid (D) TOPOLOGY: linear	
111 112	(D) TOPOLOGI: Tillear	
113	(ii) MOLECULE TYPE: peptide	
114	(11) Nobbooth 1111 Popular	
115	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
116		
117	Met Met Ile Phe Lys Lys Leu Ser Glu Lys Glu Leu Gln Lys Ile Asn	•
118	1 5 10 15	
119	and the state of t	
120	Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln 20 25 30	
121 122	20 25 30	
123	Ile Phe Thr His Arg	
124	35	
125		
126		
127	(2) INFORMATION FOR SEQ ID NO:4:	
128		
129	(i) SEQUENCE CHARACTERISTICS:	
130	(A) LENGTH: 186 base pairs	
131 132	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
132	(D) TOPOLOGY: linear	
134	(2) 2010101 1111011	
135	(ii) MOLECULE TYPE: DNA (genomic)	
136		
137		
138	(ix) FEATURE:	
139	(A) NAME/KEY: CDS (B) LOCATION: 1186	
140 141	(B) LOCATION: 1186	
142		
143	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
144		
145	ATG GAA AAG TTT ATT GAA TTA TCT TTA AAA GAA GTA ACA GCA ATT ACA	48
146	Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr	
147	1 5 10 15	
148 149	GGT GGA AAA TAT TAT GGT AAC GGT GTA CAC TGT GGA AAA CAT TCA TGT	96
150	Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys	
151	20 25 30	
152		

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/068,507A

DATE: 02/18/1999 TIME: 15:34:23

153 154 155 156	INPUT SET: S30728.rd CC GTA GAC TGG GGA ACA GCT ATT GGA AAT ATC GGA AAT AAT GCA GCT Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala 35 40 45	aw 144
157 158 159 160 161	CA AAC TGG GCC ACA GGC GGA AAC GCT GGC TGG AAT AAA TAA la Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys * 50 55 60	186
162 163	2) INFORMATION FOR SEQ ID NO:5:	
163 164 165 166 167 168	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 61 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	
169 170	(ii) MOLECULE TYPE: peptide	
171	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
172 173 174 175	Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr 1 15	
176 177 178	Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys 20 25 30	
179 180 181	Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala 35 40 45	
182 183 184 185	Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys 50 55 60	
186	(2) INFORMATION FOR SEQ ID NO:6:	
187 188 189 190 191 192 193	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 82 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
194 195 196	<pre>(ii) MOLECULE TYPE: other nucleic acid      (A) DESCRIPTION: /desc = "Promoter"</pre>	
197 198 199	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
200 201	GAGTTCTTAA CGTTAATCCG AAAAAAACTA ACGTTAATAT TAAAAAATAA GATCCGCTTG	60
202 203 204	TGAATTATGT ATAATTTGAT TN	82
205	(2) INFORMATION FOR SEQ ID NO:7:	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/068,507A

DATE: 02/18/1999 TIME: 15:34:23

INPUT SET: S30728.raw

206		
207	(i) SEQUENCE CHARACTERISTICS:	
208	(A) LENGTH: 81 base pairs	
209	(B) TYPE: nucleic acid	
210	(C) STRANDEDNESS: single	
211	(D) TOPOLOGY: linear	
212		
213	(ii) MOLECULE TYPE: other nucleic acid	
214	(A) DESCRIPTION: /desc = "Promoter"	
215		
216		
217	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
218		
219	CGCATATTAA CGTTTAACCG ATAAAGTTGA ACGTTAATAT TTTTTTTGCG CAGAAATGGT	60
220		
221	AAATTGAAGC ATAATAGTCT N	81
222		
223		
224	(2) INFORMATION FOR SEQ ID NO:8:	
225		
226	(i) SEQUENCE CHARACTERISTICS:	
227	(A) LENGTH: 82 base pairs	
228	(B) TYPE: nucleic acid	
229	(C) STRANDEDNESS: single	
230	(D) TOPOLOGY: linear	
231		
232	(ii) MOLECULE TYPE: other nucleic acid	
233	(A) DESCRIPTION: /desc = "Promoter"	
234		
235		
236	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
237		
238	GCAGCATTAA CGTTAATTTT GATAAACGTA ACGTTAATGG ATAATCATCC TGTTTACAAA	60
239		
240	TAGTGTATGA CATAATTAAG TN	82
241		
242		
243	(2) INFORMATION FOR SEQ ID NO:9:	
244		
245	(i) SEQUENCE CHARACTERISTICS:	
246	(A) LENGTH: 81 base pairs	
247	(B) TYPE: nucleic acid	
248	(C) STRANDEDNESS: single	
249	(D) TOPOLOGY: linear	
250		
25		

## SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/09/068,507A

DATE: 02/18/1999

TIME: 15:34:24

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PAGE: 1

### RAW SEQUENCE LISTING PATENT APPLICATION US/09/068,507A

DATE: 02/18/1999 TIME: 13:50:38

INPUT SET: S30728.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1		SEQUENCE LISTING
2		eneral Information:  APPLICANT: EIJSINK, VINCENT G.H.  BRURBERG, MAY B.  Does Not Comply  Corrected Diskette Needec
3	(1) G	eneral Information:
4	(:)	A DDI TONNEL EL ICINY WINCENT G. H.
5 6	(1)	APPLICANT: EIJSINK, VINCENT G.H.  BRURBERG, MAY B.
7		NES, INGOLF F.
8		,
9	(ii)	TITLE OF INVENTION: EXPRESSION SYSTEM IN MICROORGANISM AND
10		ITS USE FOR EXPRESSING HETEROLOGOUS AND HOMOLOGOUS
11		PROTEINS
12 13	(:::)	NUMBER OF SEQUENCES: 12
14	(111)	MONDER OF SEGOENCES
15	(iv)	CORRESPONDENCE ADDRESS:
16		(A) ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
17		(B) STREET: PO BOX 747
18		(C) CITY: FALLS CHURCH (D) STATE: VA
19 20		(E) COUNTRY: USA
21		(F) ZIP: 22040-0747
22		
23	(v)	COMPUTER READABLE FORM:
24		(A) MEDIUM TYPE: Floppy disk
25		(B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 27		(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28		(2)
29	(vi)	CURRENT APPLICATION DATA:
30		(A) APPLICATION NUMBER:
31		(B) FILING DATE:
32 33		(C) CLASSIFICATION:
34	(viii)	ATTORNEY/AGENT INFORMATION:
35	, ,	(A) NAME: MURPHY JR., GERLAD M.
36		(B) REGISTRATION NUMBER: 28,977
37		(C) REFERENCE/DOCKET NUMBER: 1380-0122P
38	( + )	TELECOMMUNICATION INFORMATION:
39 40	(IX)	(A) TELEPHONE: 703-205-8000
41		(B) TELEFAX: 703-205-8050
42		
43		
44	(2) INF	ORMATION FOR SEQ ID NO:1:
45 46	(;)	SEQUENCE CHARACTERISTICS:
40	(1)	DIROTHOL CHARGOLINE TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO THE TOTAL T

#### (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: 37 (A) LENGTH: (38 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: Met Met Ile Phe Lys Lys Leu Ser Glu Lys Glu Leu Gln Lys Ile Asn Gly Gly Met Ala Gly Asn Ser Ser Asn Phe Ile His Lys Ile Lys Gln Ile Phe Thr His Arq 35 (2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 186 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: ATG GAA AAG TTT ATT GAA TTA TCT TTA AAA GAA GTA ACA GCA ATT ACA 48 Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr 1 GGT GGA AAA TAT TAT GGT AAC GGT GTA CAC TGT GGA AAA CAT TCA TGT 96 Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys 20 ACC GTA GAC TGG GGA ACA GCT ATT GGA AAT ATC GGA AAT AAT GCA GCT 144 Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala 35 GCA AAC TGG GCC ACA GGC GGA AAC GCT GGC TGG AAT AAA TAA 186 Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys 50 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Lys Phe Ile Glu Leu Ser Leu Lys Glu Val Thr Ala Ile Thr 1 5 10 15

Gly Gly Lys Tyr Tyr Gly Asn Gly Val His Cys Gly Lys His Ser Cys 20 25 30

Thr Val Asp Trp Gly Thr Ala Ile Gly Asn Ile Gly Asn Asn Ala Ala

Ala Asn Trp Ala Thr Gly Gly Asn Ala Gly Trp Asn Lys
50 55 60